

Table S1

*Blastocystis*-positive samples, percentage of 18S sequences *Blastocystis*, and subtypes of *Blastocystis* identified.

<b>HMP Sample</b>	<b>% 18S sequences <i>Blastocystis</i></b>	<b>Subtype</b>
Vol.241676.3	21.15%	ST3
Vol.241710.1	100.0%	ST2
Vol.241710.2	100.0%	ST2
Vol.241711.1	100.0%	ST1
Vol.241711.2	100.0%	ST1
Vol.241711.3	100.0%	ST1
Vol.241712.1	68.2%	ST3
Vol.241721.3	0.2%	ST2
Vol.241754.1	100.0%	ST3
Vol.241754.2	100.0%	ST3
Vol.241754.3	100.0%	ST1
Vol.241755.3	0.03%	ST1
Vol.241776.3	74.6%	ST3
Vol.241780.2	100.0%	ST3
Vol.241780.3	100.0%	ST3
Vol.241849.1	93.1%	ST3
Vol.241849.2	99.9%	ST3
Vol.241849.3	100.0%	ST3
Vol.285223.1	3.3%	ST1

Figure S1

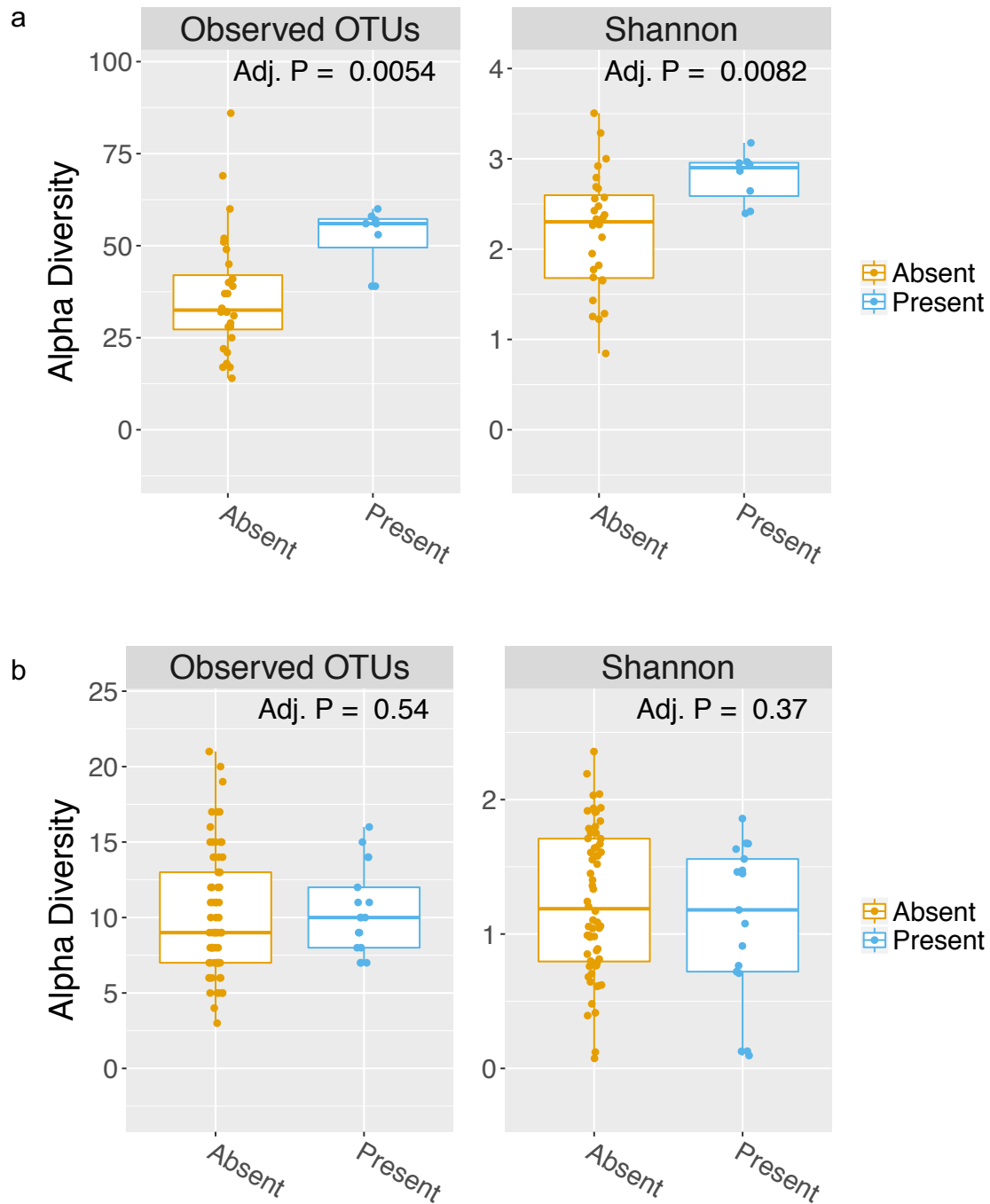


Figure S1: Alpha diversity of samples in which *Blastocystis* was (blue) or was not (yellow) detected. **a** 16S rRNA gene alpha diversity from dataset rarefied to 735 reads. Due to small sample size, the statistical significance varied greatly depending on the rarefaction and randomly chosen samples. **b** ITS2 alpha diversity from dataset rarefied to 4043 reads.